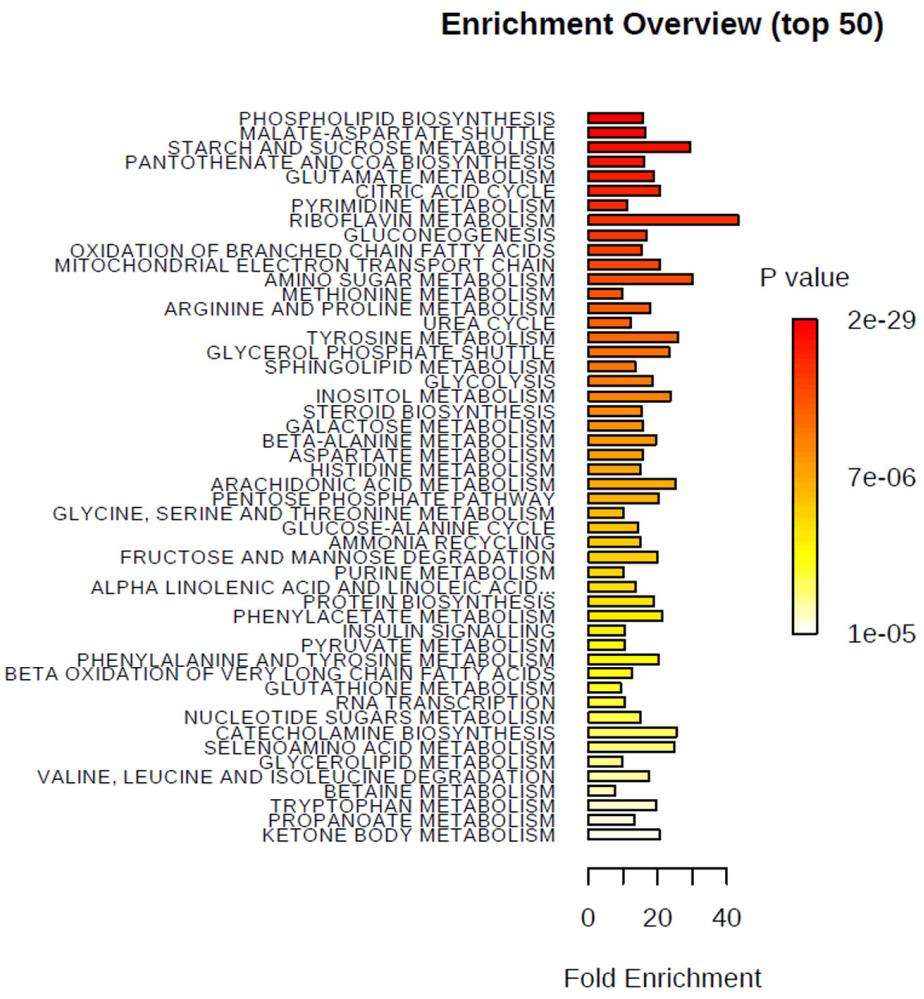
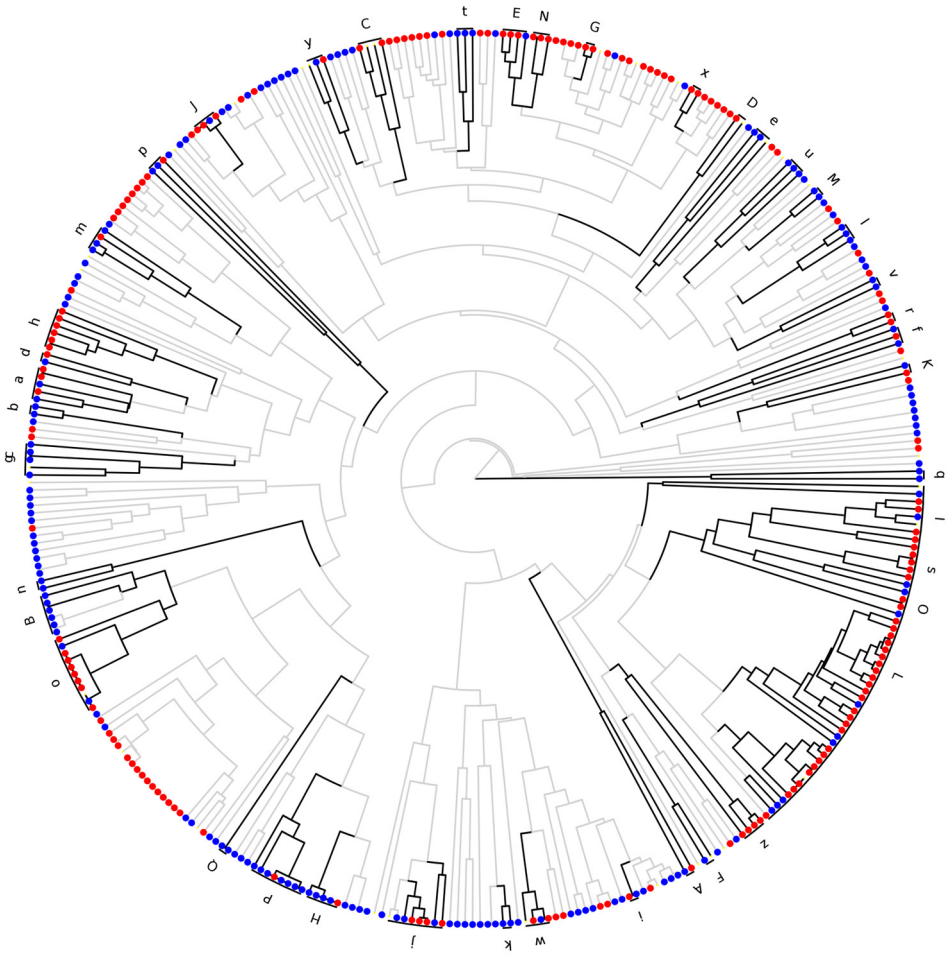
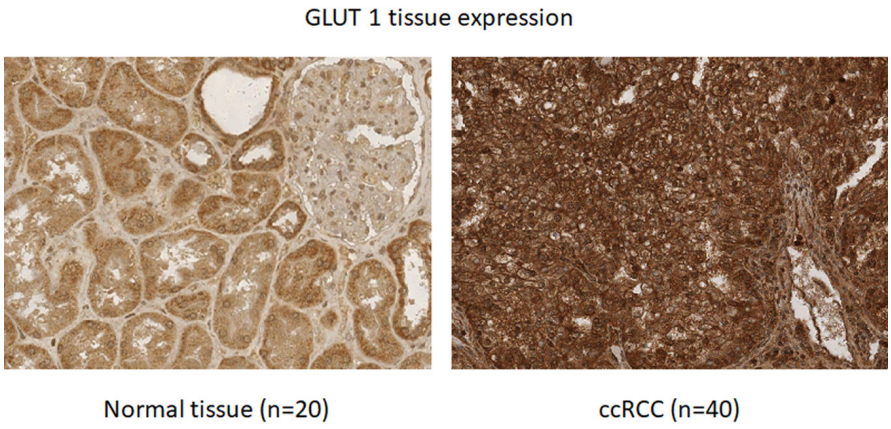
SUPPLEMENTARY FIGURES



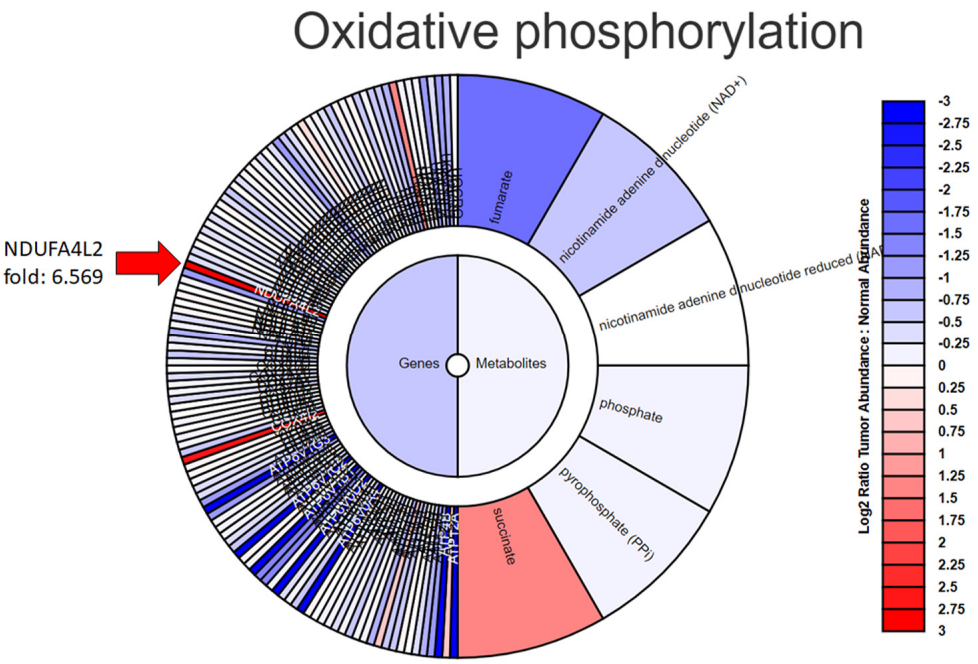
Supplementary Figure 1. Metabolite set enrichment overview performed in MetaboAnalyst 3.0



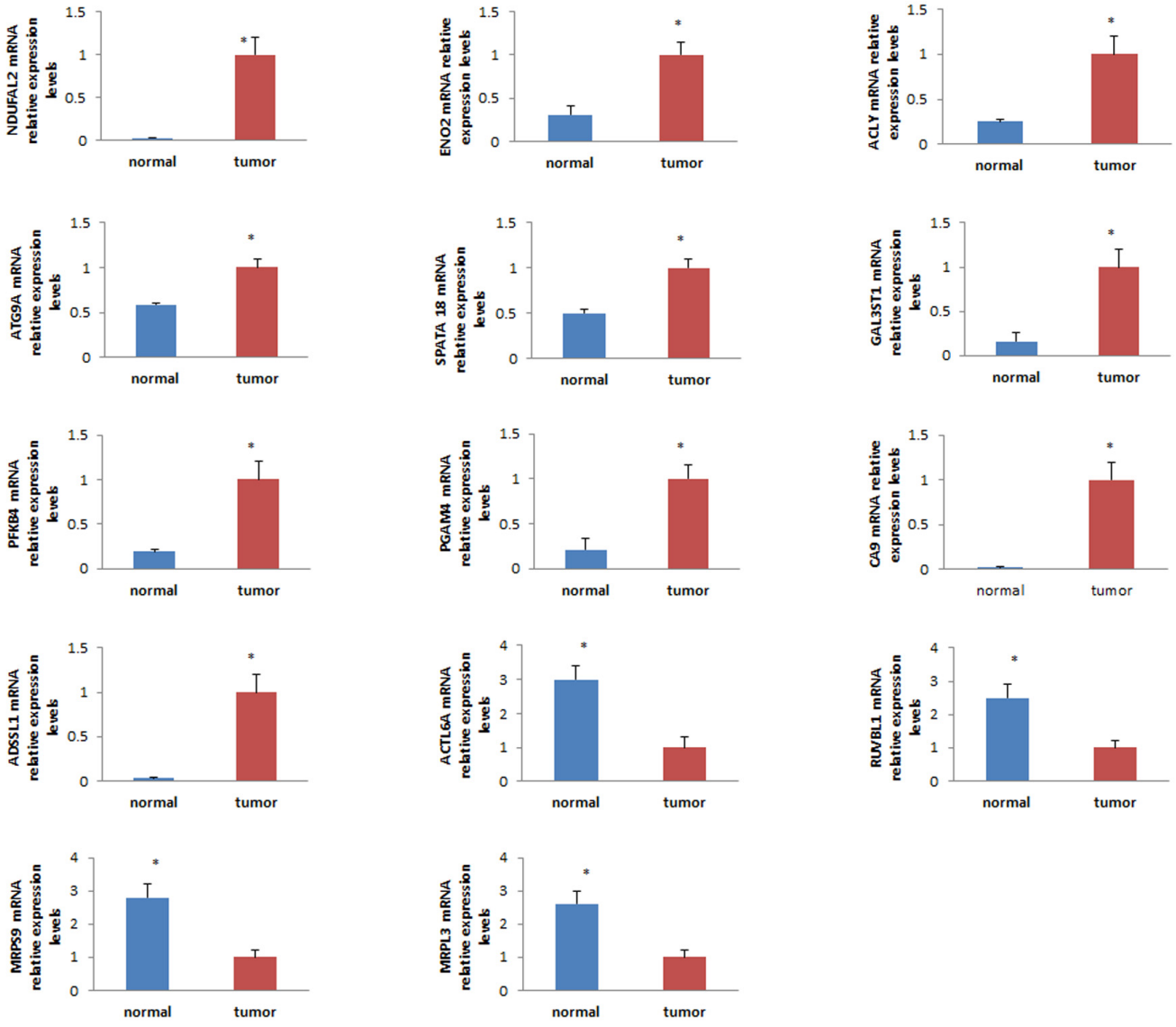
Supplementary Figure 2. Tanimoto chemical similarity mapping of all identified metabolites in ccRCC. Clusters are defined by comparing within- versus between group similarities, forming a clustered chemical similarity tree. Dark black lines indicate boundaries of clusters significantly different in tumor versus normal tissue ($p<0.05$). Cluster letter labels are detailed in Supplementary Table 2. Increased metabolites in ccRCC are labeled as red nodes. Decreased metabolites are blue nodes.



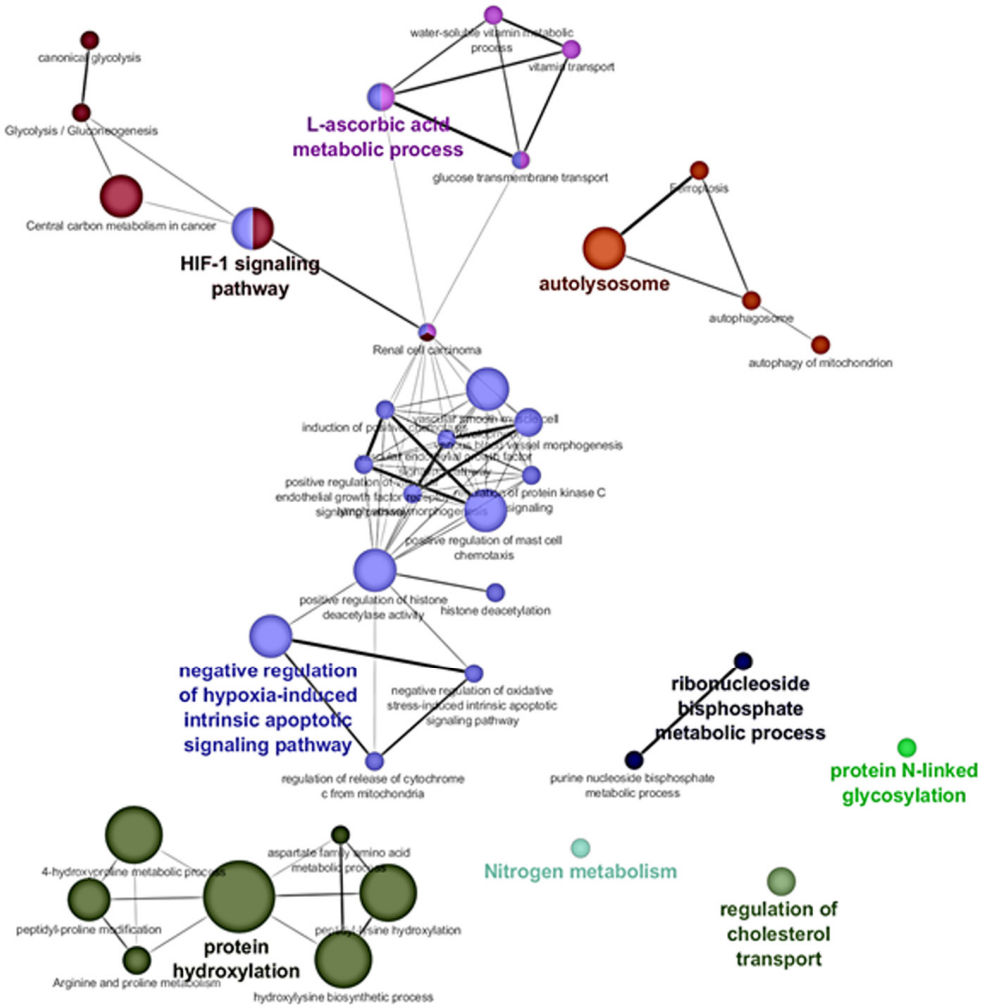
Supplementary Figure 3. Glut1 expression in normal (n=20) and ccRCC (n=40) specimens.



Supplementary Figure 4. Exploration of the "Metabologram" Data Portal. The changes in the "Oxidative phosphorylation" metabolism pathway are shown in both transcripts and metabolites when comparing tumors to adjacent normal kidney tissues.



Supplementary Figure 5. Gene expression by real-time PCR.



Supplementary Figure 6. Enriched GO network groups using ClueGO for GSE117890 dataset analysis. Biological processes (GO category) are visualized (kappa score ≥ 0.3) as a functional grouped network and only the most significant interactions are shown. Each node represents a biological process. Edges represent connections between the nodes and the length of each edge reflects the relatedness of two processes.